



Atty. Dkt. No. 081356-0111

#21
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9/2/03

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Susmu KAJIWARA et al.
Title: A DNA CHAIN USEFUL FOR
INCREASING PRODUCTION OF
CAROTENOIDS
Appl. No.: 08/737,319
Filing Date: 11/12/1996
Examiner: K. Kerr
Art Unit: 1652

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TRANSMITTAL OF FORMAL DRAWINGS

Commissioner for Patents
PO Box 1450
Alexandria, Virginia 22313-1450

ATTENTION: DRAWING REVIEW BRANCH

Sir:

Transmitted herewith are the formal drawings (14 sheets, Figures 1-14) for the above-identified application. The Official Draftsperson is respectfully requested to approve these drawings for entry into the application.

Respectfully submitted,

Date August 7, 2003

FOLEY & LARDNER
Customer Number: 22428

22428

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PATENT TRADEMARK OFFICE

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By

Stephen A. Bent
Attorney for Applicant
Registration No. 29,768

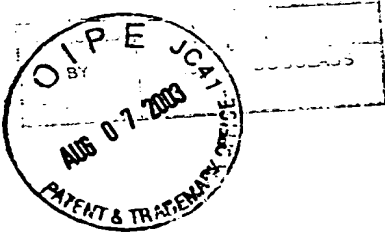
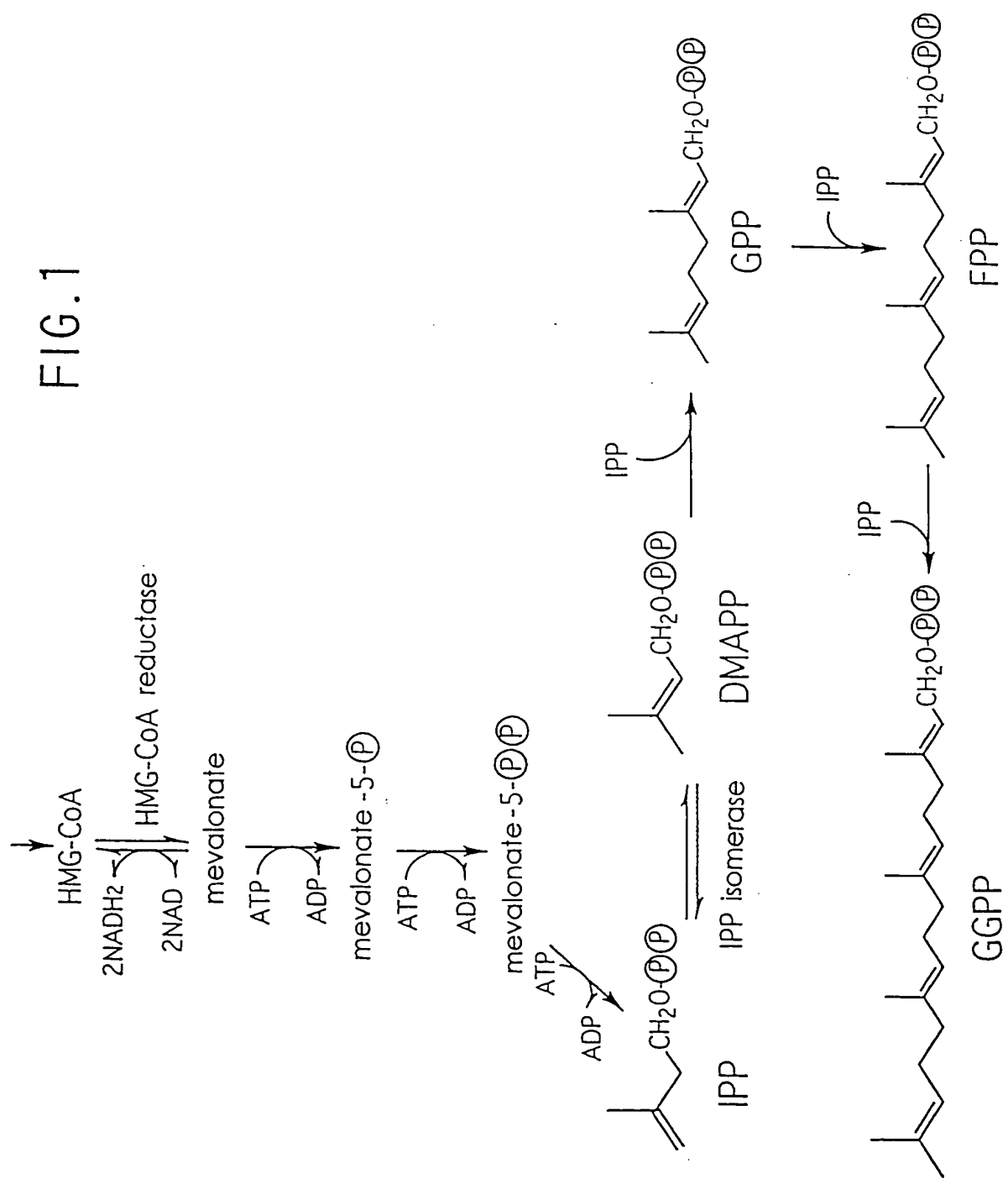
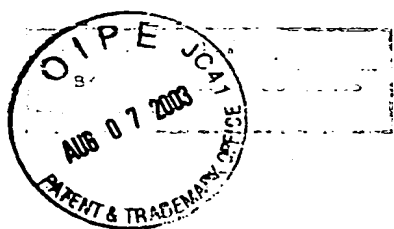


FIG. 1

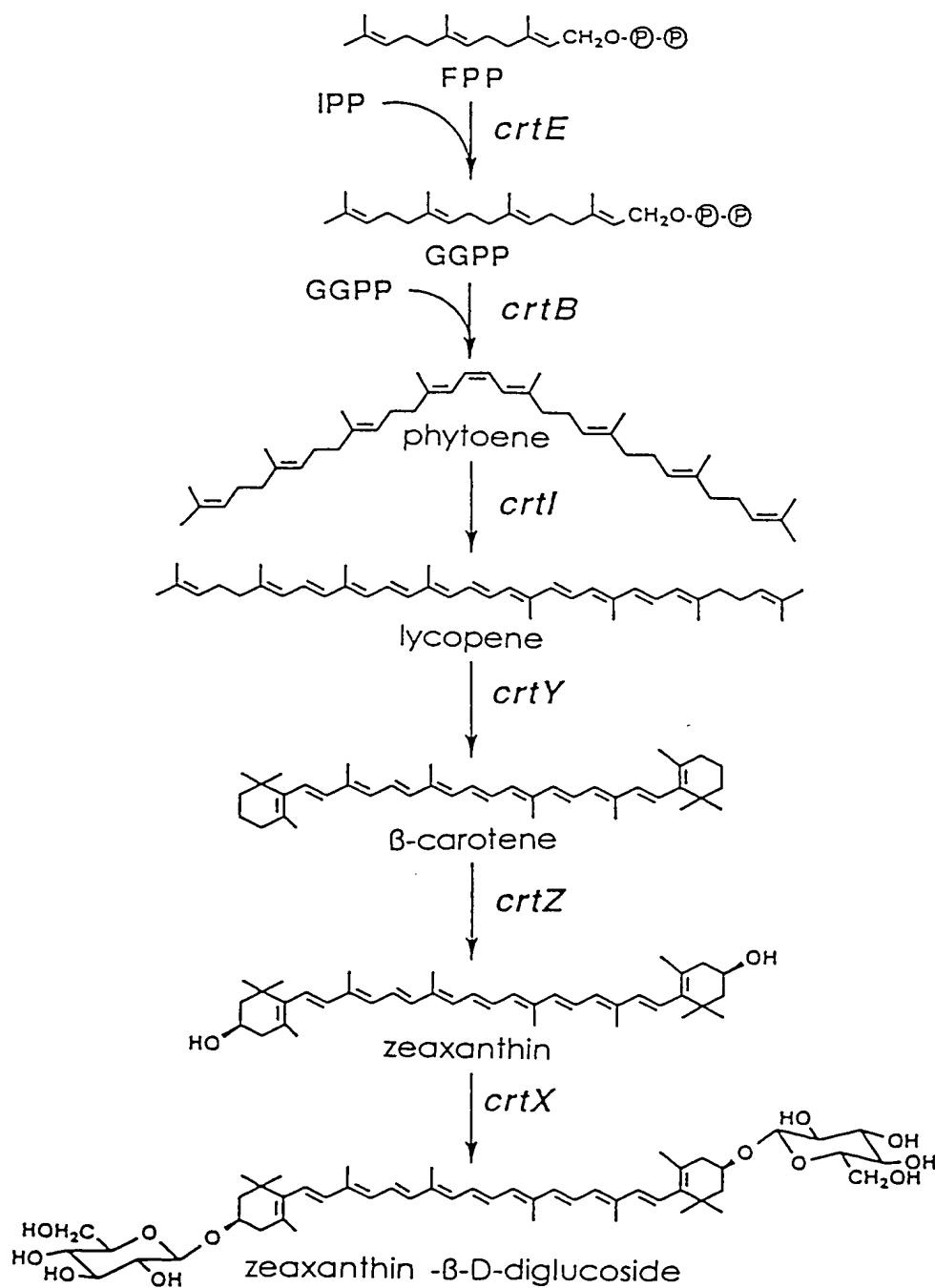




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FIG.2



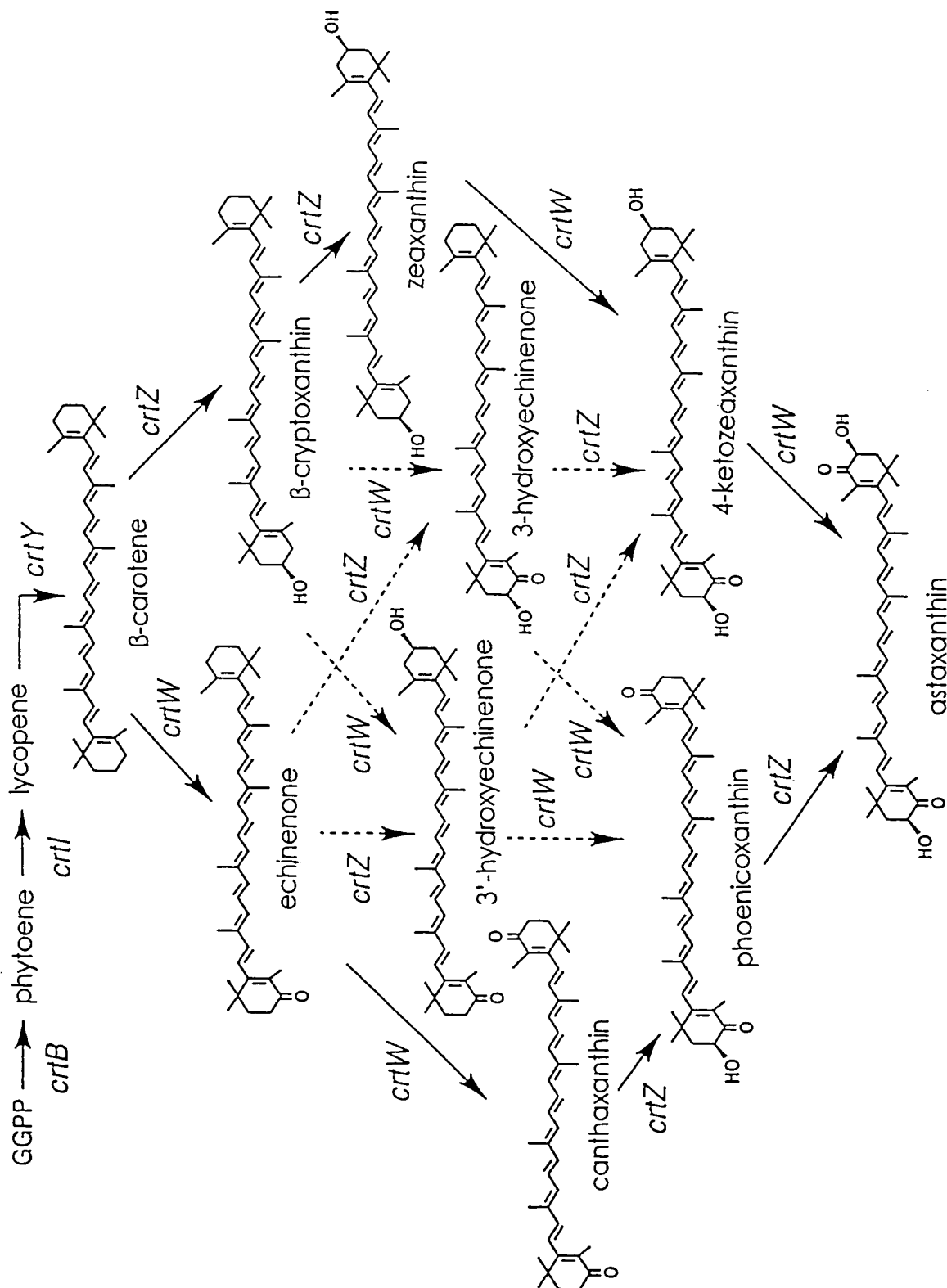


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FIG. 3



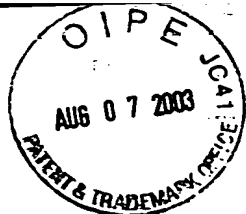


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FIG. 4

A
↓

9	18	27	36	45	54
ATG TCC ATG CCC AAC ATT GTT CCC CCC GCC GAG GTC CGA ACC GAA GGA CTC AGT					
Met Ser Met Pro Asn Ile Val Pro Pro Ala Glu Val Arg Thr Glu Gly Leu Ser					
					18
63	72	81	90	99	108
TTA GAA GAG TAC GAT GAG GAG CAG GTC AGG CTG ATG GAG GAG CGA TGT ATT CTT					
Leu Glu Glu Tyr Asp Glu Glu Gln Val Arg Leu Met Glu Glu Arg Cys Ile Leu					
					36
117	126	135	144	153	162
GTT AAC CCG GAC GAT GTG GCC TAT GGA GAG GCT TCG AAA AAG ACC TGC CAC TTG					
Val Asn Pro Asp Asp Val Ala Tyr Gly Glu Ala Ser Lys Lys Thr Cys His Leu					
					54
171	180	189	198	207	216
ATG TCC AAC ATC AAC GCG CCC AAG GAC CTC CTC CAC CGA GCA TTC TCC GTG TTT					
Met Ser Asn Ile Asn Ala Pro Lys Asp Leu Leu His Arg Ala Phe Ser Val Phe					
					72
225	234	243	252	261	270
CTC TTC CGC CCA TCG GAC GGA GCA CTC CTG CTT CAG CGA AGA GCG GAC GAG AAG					
Leu Phe Arg Pro Ser Asp Gly Ala Leu Leu Leu Gln Arg Arg Ala Asp Glu Lys					
					90
279	288	297	306	315	324
ATT ACG TTC CCT GGA ATG TGG ACC AAC ACG TGT TGC AGT CAT CCT TTG AGC ATC					
Ile Thr Phe Pro Gly Met Trp Thr Asn Thr Cys Cys Ser His Pro Leu Ser Ile					
					108
333	342	351	360	369	378
AAG GGC GAG GTT GAA GAG GAG AAC CAG ATC GGT GTT CGA CGA GCT GCG TCC CGA					
Lys Gly Glu Val Glu Glu Glu Asn Gln Ile Gly Val Arg Arg Ala Ala Ser Arg					
					126
387	396	405	414	423	432
AAG TTG GAG CAC GAG CTT GGC GTG CCT ACA TCG TCG ACT CCG CCC GAC TCG TTC					
Lys Leu Glu His Glu Leu Gly Val Pro Thr Ser Ser Thr Pro Pro Asp Ser Phe					
					144
441	450	459	468	477	486
ACC TAC CTC ACT AGG ATA CAT TAC CTC GCT CCG AGT GAC GGA CTC TGG GGA GAA					
Thr Tyr Leu Thr Arg Ile His Tyr Leu Ala Pro Ser Asp Gly Leu Trp Gly Glu					
					162
495	504	513	522	531	540
CAC GAG ATC GAC TAC ATT CTC TTC TCA ACC ACA CCT ACA GAA CAC ACT GGA AAC					
His Glu Ile Asp Tyr Ile Leu Phe Ser Thr Thr Pro Thr Glu His Thr Gly Asn					
					180
549	558	567	576	585	594
CCT AAC GAA GTC TCT GAC ACT CGA TAT GTC ACC AAG CCC GAG CTC CAG GCG ATG					
Pro Asn Glu Val Ser Asp Thr Arg Tyr Val Thr Lys Pro Glu Leu Gln Ala Met					
					198



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FIG. 5

603	612	621	630	639	648
TTT GAG GAC GAG TCT AAC TCA TTT ACC CCT TGG TTC AAG TTG ATT GCC CGA GAC					
Phe Glu Asp Glu Ser Asn Ser Phe Thr Pro Trp Phe Lys Leu Ile Ala Arg Asp					
					216
657	666	675	684	693	702
TTC CTG TTT GGC TGG TGG GAT CAA CTT CTC GCC AGA CGA AAT GAA AAG GGT GAG					
Phe Leu Phe Gly Trp Trp Asp Gln Leu Leu Ala Arg Arg Asn Glu Lys Gly Glu					
					234
711	720	729	738	747	756
GTC GAT GCC AAA TCG TTG GAG GAT CTC TCG GAC AAC AAA GTC TGG AAG ATG TAG					
Val Asp Ala Lys Ser Leu Glu Asp Leu Ser Asp Asn Lys Val Trp Lys Met ***					
					251
					B



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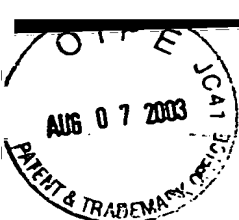
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FIG. 6

C
↓

9	18	27	36	45	54
ATG CAG CTG CTT GCC GAG GAC CGC ACA GAC CAT ATG AGG GGT GCA AGT ACC TGG					
Met Gln Leu Leu Ala Glu Asp Arg Thr Asp His Met Arg Gly Ala Ser Thr Trp					
					18
63	72	81	90	99	108
GCA GGC GGG CAG TCG CAG GAT GAG CTG ATG CTG AAG GAC GAG TGC ATC TTG GTG					
Ala Gly Gly Gln Ser Gln Asp Glu Leu Met Leu Lys Asp Glu Cys Ile Leu Val					
					36
117	126	135	144	153	162
GAT GCT GAC GAC AAC ATT ACA GGC CAT GTC AGC AAG CTG GAG TGC CAC AAG TTC					
Asp Ala Asp Asp Asn Ile Thr Gly His Val Ser Lys Leu Glu Cys His Lys Phe					
					54
171	180	189	198	207	216
CTA CCA CAT CAG CCT GCA GGC CTG CTG CAC CGG GCC TTC TCT GTA TTC CTG TTT					
Leu Pro His Gln Pro Ala Gly Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe					
					72
225	234	243	252	261	270
GAC GAC CAG GGG CGA CTG CTG CTG CAA CAG CGT GCA CGA TCA AAA ATC ACA TTC					
Asp Asp Gln Gly Arg Leu Leu Leu Gln Gln Arg Ala Arg Ser Lys Ile Thr Phe					
					90
279	288	297	306	315	324
CCC AGT GTG TGG ACC AAC ACC TGC TGC AGC CAC CCT CTA CAT GGG CAG ACC CCA					
Pro Ser Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu His Gly Gln Thr Pro					
					108
333	342	351	360	369	378
GAT GAG GTG GAC CAA CTA AGC CAG GTG GCC GAC GGC ACA GTA CCT GGC GCA AAG					
Asp Glu Val Asp Gln Leu Ser Gln Val Ala Asp Gly Thr Val Pro Gly Ala Lys					
					126
387	396	405	414	423	432
GCT GCT GCC ATC CGC AAG TTG GAG CAC GAG CTG GGG ATA CCA GCG CAC CAG CTG					
Ala Ala Ala Ile Arg Lys Leu Glu His Glu Leu Gly Ile Pro Ala His Gln Leu					
					144
441	450	459	468	477	486
CCG GCC AGC GCG TTT CGC TTC CTC ACG CGT TTG CAC TAC TGC GCC GCG GAC GTG					
Pro Ala Ser Ala Phe Arg Phe Leu Thr Arg Leu His Tyr Cys Ala Ala Asp Val					
					162
495	504	513	522	531	540
CAG CCG GCT GCG ACA CAA TCA GCA CTC TGG GGC GAG CAC GAA ATG GAC TAC ATC					
Gln Pro Ala Ala Thr Gln Ser Ala Leu Trp Gly Glu His Glu Met Asp Tyr Ile					
					180
549	558	567	576	585	594
TTA TTC ATC CGG GCC AAC GTC ACC CTT GCG CCC AAC CCT GAC GAG GTG GAC GAA					
Leu Phe Ile Arg Ala Asn Val Thr Leu Ala Pro Asn Pro Asp Glu Val Asp Glu					
					198



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FIG. 7

603	612	621	630	639	648
GTC AGG TAC GTG ACG CAG GAG GAG CTG CGG CAG ATG ATG CAG CCG GAC AAT GGG					
Val Arg Tyr Val Thr Gln Glu Glu Leu Arg Gln Met Met Gln Pro Asp Asn Gly					
					216
657	666	675	684	693	702
TTG CAA TGG TCG CCG TGG TTT CGC ATC ATC GCC GCG CGC TTC CTT GAG CGC TGG					
Leu Gln Trp Ser Pro Trp Phe Arg Ile Ile Ala Ala Arg Phe Leu Glu Arg Trp					
					234
711	720	729	738	747	756
TGG GCT GAC CTA GAC GCG GCC CTG AAC ACT GAC AAA CAC GAG GAT TGG GGA ACG					
Trp Ala Asp Leu Asp Ala Ala Leu Asn Thr Asp Lys His Glu Asp Trp Gly Thr					
					252
765	774	780			
GTG CAT CAC ATC AAC GAA GCG TGA					
Val His His Ile Asn Glu Ala ***					
		259			
		D			



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FIG. 8

E
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9	18	27	36	45	54
ATG ACT GCC GAC AAC AAT AGT ATG CCC CAT GGT GCA GTA TCT AGT TAC GCC AAA					
Met Thr Ala Asp Asn Asn Ser Met Pro His Gly Ala Val Ser Ser Tyr Ala Lys					
					18
63	72	81	90	99	108
TTA GTG CAA AAC CAA ACA CCT GAA GAC ATT TTG GAA GAG TTT CCT GAA ATT ATT					
Leu Val Gln Asn Gln Thr Pro Glu Asp Ile Leu Glu Glu Phe Pro Glu Ile Ile					
					36
117	126	135	144	153	162
CCA TTA CAA CAA AGA CCT AAT ACC CGA TCT AGT GAG ACG TCA AAT GAC GAA AGC					
Pro Leu Gln Gln Arg Pro Asn Thr Arg Ser Ser Glu Thr Ser Asn Asp Glu Ser					
					54
171	180	189	198	207	216
GGA GAA ACA TGT TTT TCT GGT CAT GAT GAG GAG CAA ATT AAG TTA ATG AAT GAA					
Gly Glu Thr Cys Phe Ser Gly His Asp Glu Glu Gln Ile Lys Leu Met Asn Glu					
					72
225	234	243	252	261	270
AAT TGT ATT GTT TTG GAT TGG GAC GAT AAT GCT ATT GGT GCC GGT ACC AAG AAA					
Asn Cys Ile Val Leu Asp Trp Asp Asp Asn Ala Ile Gly Ala Gly Thr Lys Lys					
					90
279	288	297	306	315	324
GTT TGT CAT TTA ATG GAA AAT ATT GAA AAG GGT TTA CTA CAT CGT GCA TTC TCC					
Val Cys His Leu Met Glu Asn Ile Glu Lys Gly Leu Leu His Arg Ala Phe Ser					
					108
333	342	351	360	369	378
GTC TTT ATT TTC AAT GAA CAA GGT GAA TTA CTT TTA CAA CAA AGA GCC ACT GAA					
Val Phe Ile Phe Asn Glu Gln Gly Glu Leu Leu Leu Gln Gln Arg Ala Thr Glu					
					126
387	396	405	414	423	432
AAA ATA ACT TTC CCT GAT CTT TGG ACT AAC ACA TGC TGC TCT CAT CCA CTA TGT					
Lys Ile Thr Phe Pro Asp Leu Trp Thr Asn Thr Cys Cys Ser His Pro Leu Cys					
					144
441	450	459	468	477	486
ATT GAT GAC GAA TTA GGT TTG AAG GGT AAG CTA GAC GAT AAG ATT AAG GGC GCT					
Ile Asp Asp Glu Leu Gly Leu Lys Gly Lys Leu Asp Asp Lys Ile Lys Gly Ala					
					162
495	504	513	522	531	540
ATT ACT GCG GCG GTG AGA AAA CTA GAT CAT GAA TTA GGT ATT CCA GAA GAT GAA					
Ile Thr Ala Ala Val Arg Lys Leu Asp His Glu Leu Gly Ile Pro Glu Asp Glu					
					180



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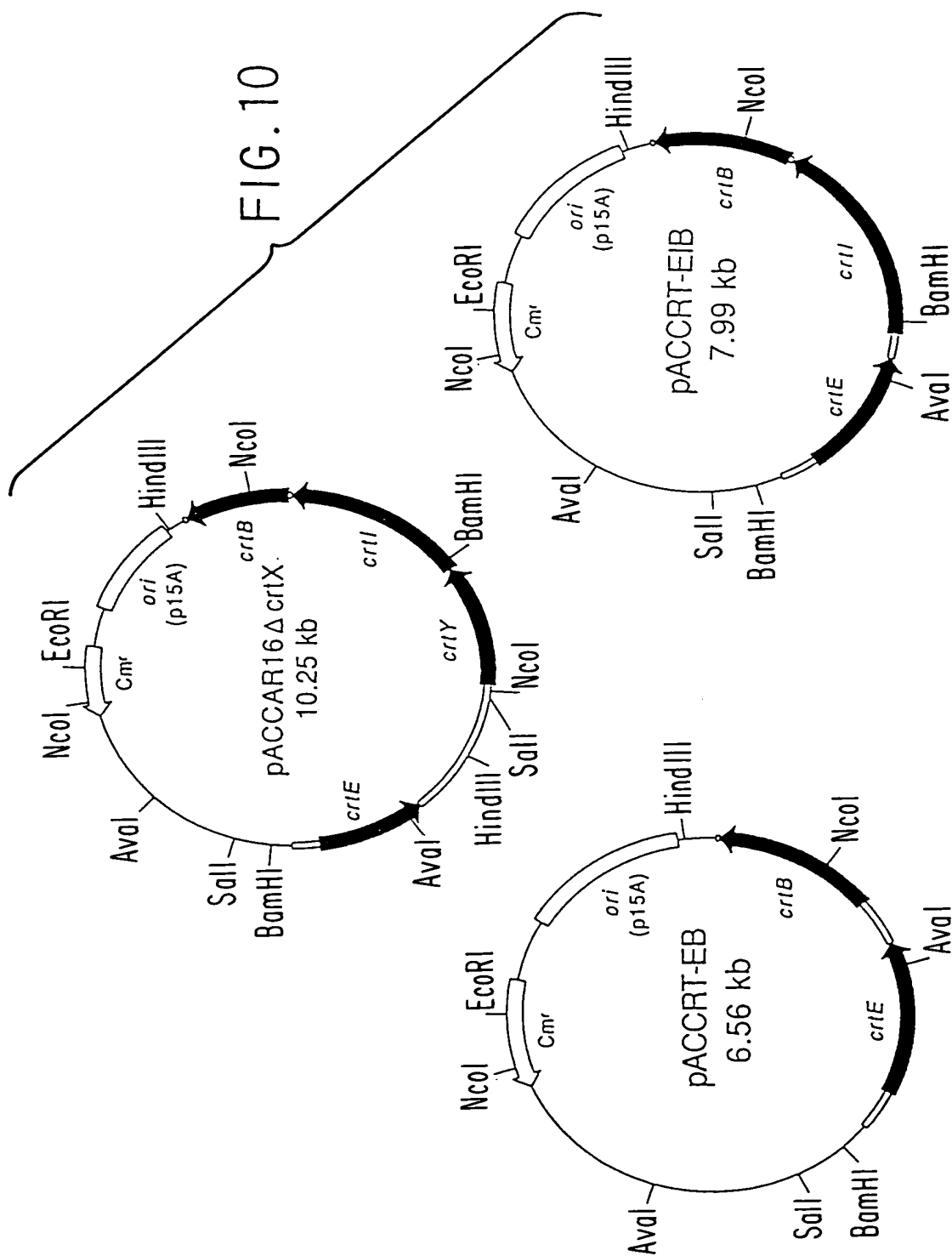
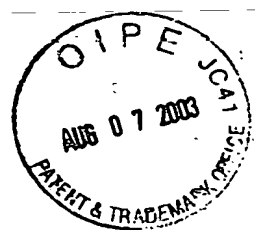
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FIG. 9

549	558	567	576	585	594
ACT AAG ACA AGG GGT AAG TTT CAC TTT TTA AAC AGA ATC CAT TAC ATG GCA CCA					
Thr Lys Thr Arg Gly Lys Phe His Phe Leu Asn Arg Ile His Tyr Met Ala Pro					
					198
603	612	621	630	639	648
AGC AAT GAA CCA TGG GGT GAA CAT GAA ATT GAT TAC ATC CTA TTT TAT AAG ATC					
Ser Asn Glu Pro Trp Gly Glu His Glu Ile Asp Tyr Ile Leu Phe Tyr Lys Ile					
					216
657	666	675	684	693	702
AAC GCT AAA GAA AAC TTG ACT GTC AAC CCA AAC GTC AAT GAA GTT AGA GAC TTC					
Asn Ala Lys Glu Asn Leu Thr Val Asn Pro Asn Val Asn Glu Val Arg Asp Phe					
					234
711	720	729	738	747	756
AAA TGG GTT TCA CCA AAT GAT TTG AAA ACT ATG TTT GCT GAC CCA AGT TAC AAG					
Lys Trp Val Ser Pro Asn Asp Leu Lys Thr Met Phe Ala Asp Pro Ser Tyr Lys					
					252
765	774	783	792	801	810
TTT ACG CCT TGG TTT AAG ATT ATT TGC GAG AAT TAC TTA TTC AAC TGG TGG GAG					
Phe Thr Pro Trp Phe Lys Ile Ile Cys Glu Asn Tyr Leu Phe Asn Trp Trp Glu					
					270
819	828	837	846	855	864
CAA TTA GAT GAC CTT TCT GAA GTG GAA AAT GAC AGG CAA ATT CAT AGA ATG CTA					
Gln Leu Asp Asp Leu Ser Glu Val Glu Asn Asp Arg Gln Ile His Arg Met Leu					
					288
867					
TAA					

F



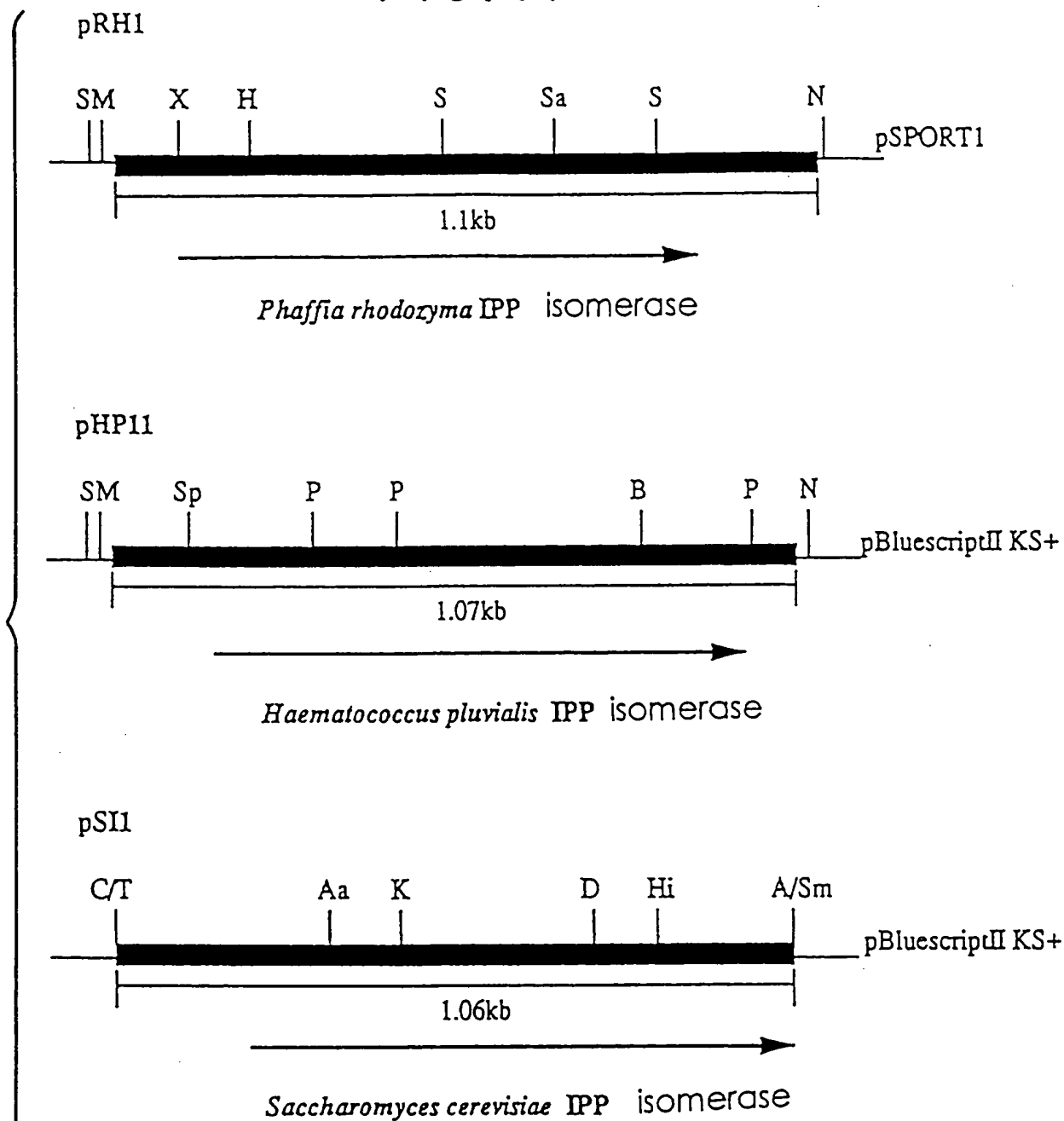


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FIG.11



Aa: AatII, A: AccII, B:BssHII, D:DraI, Hi:HincII,
H:HpaI, K:KpnI, M:MluI, N:NotI, P:PstI, Sa:SacI,
S:SalI, Sp:SphI, X:XbaI

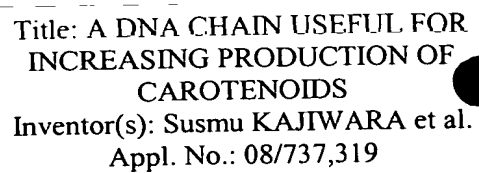


Figure 1 is a line graph showing the absorbance at 650 nm over time (hr) for four different L-lysine formulations: L:control (filled square), L:pRH1 (open square), L:pHP11 (open circle), and L:pSI1 (open triangle). The x-axis represents time in hours, ranging from 0 to 30. The y-axis represents absorbance at 650 nm, ranging from 0 to 5. All formulations show a rapid increase in absorbance within the first 10 hours, followed by a slower increase. The L:pHP11 formulation shows the highest absorbance values, while L:control shows the lowest.

time(hr)	L:control	L:pRH1	L:pHP11	L:pSI1
0	0.0	0.0	0.0	0.0
2	0.2	0.2	0.2	0.2
4	0.8	0.8	0.9	0.9
8	2.2	2.2	2.3	2.3
12	2.8	2.8	3.0	2.9
24	4.2	4.1	4.6	4.3
28	4.3	4.2	4.6	4.4

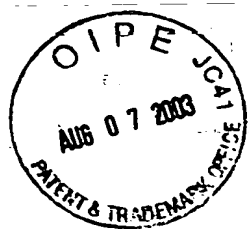
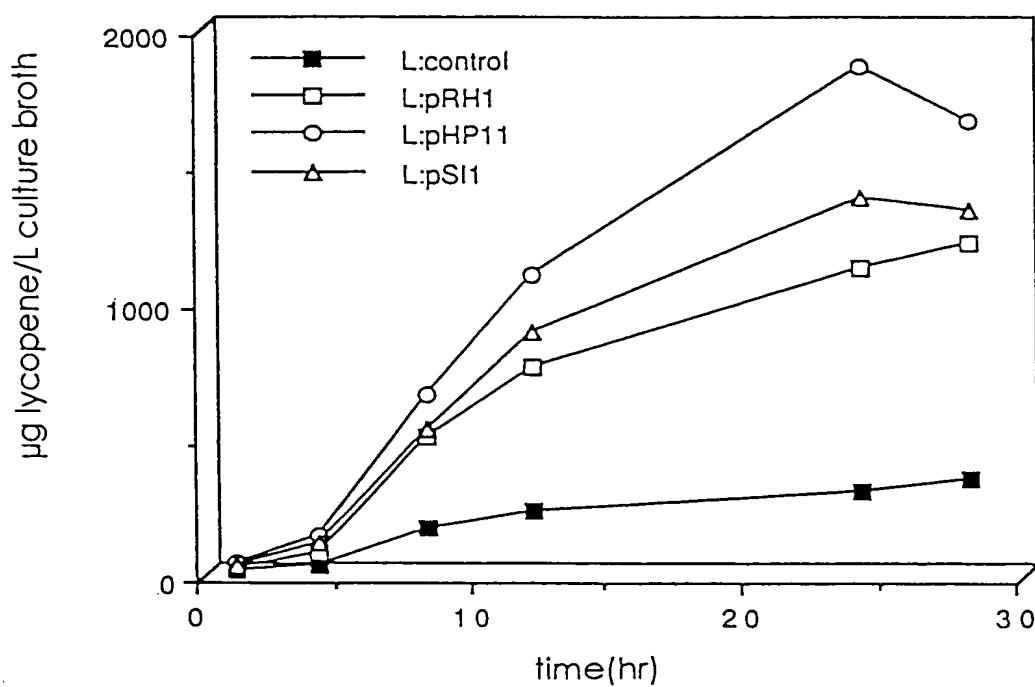
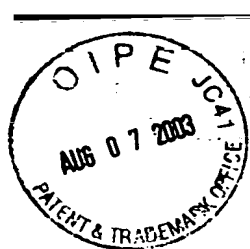


FIG.13





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FIG.14

E.coli	µg carotene/g dry weight	production ratio
L: control	228	1
L: pRH1	825	3.6
L: pHP11	1029	4.5
L: pSI1	859	3.8
β: control	488	1
β: pRH1	709	1.5
P: control	246	1
P: pRH1	413	1.7
P: pHP11	504	2.1